



#8/43

SEQUENCE LISTING

<110> Manners, John M.
Marcus, John Paul
Goulter, Kenneth C.
Green, Jodie L.

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<151> 1997-12-22

<150> AU PO 4275

<151> 1996-12-20

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Arg Gln Gln Glu Ser Asp Pro Arg Gln Gln Gln Tyr Cys Gln Arg Arg
 50          55          60
Cys Lys Glu Ile Cys Glu Glu Glu Glu Glu Tyr Asn Arg Gln Arg Asp
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Pro Gln Gln Gln Tyr Glu Gln Cys Gln Lys Arg Cys Gln Arg Arg Glu
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Thr Glu Pro Arg His Met Gln Ile Cys Gln Gln Arg Cys Glu Arg Arg
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Glu Glu Gly His Ile Ser Val Leu Glu Asn Phe Tyr Gly Arg Ser Lys		
225	230	235
Leu Leu Arg Ala Leu Lys Asn Tyr Arg Leu Val Leu Leu Glu Ala Asn		
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Pro Asn Ala Phe Val Leu Pro Thr His Leu Asp Ala Asp Ala Ile Leu		
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Leu Val Ile Gly Gly Arg Gly Ala Leu Lys Met Ile His Arg Asp Asn		
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Arg Glu Ser Tyr Asn Leu Glu Cys Gly Asp Val Ile Arg Ile Pro Ala		
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Gly Thr Thr Phe Tyr Leu Ile Asn Arg Asp Asn Asn Glu Arg Leu His		
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Ile Ala Lys Phe Leu Gln Thr Ile Ser Thr Pro Gly Gln Tyr Lys Glu		
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ccactgtact ccaacaaata cggtaagcc tacgaagtca aacctgagga ctacaggcaa 1320
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cccttcttca acactagggt tacaaggtg gtagtggtgg ctagtggaga ggcagatgtg 1440
gaaatggcat gccctcactt gtcgggaaga cacggcgccg gcggtggagg gaaaaggcat 1500
gaggaggaag aggaggtgca ctatgagcag gttagagcac gtttgtcgaa gagagaggcc 1560
attgttggtc tggcaggtca tccgctcgtc ttcgtttcat ccggaaacga aaacctgctg 1620
ctttttgcat ttggaatcaa tgccaaaaac aaccacgaga acttcctcgc ggggagagag 1680
aggaacgtgc tgcagcagat agagccacag gcaatggagc tagcgtttgc cgcttcaagg 1740
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cagcaccagc aacagtcgcc ccgctccacc aagcaacaac agcctctcgt ctccattctg 1860
gacttcgttg gcttctaaag ttctacaaaa aagagtgtgt tatgtagtat aggttagtag 1920
ctcctagctc ggtgtatgag agtggttaaga gactaagacg ctaaatccct aagtaactaa 1980
cctggcgagc ttgcgtgtat gcaaataaag aggaacagct ttccaacttt agaaagctct 2040
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<210> 7
<211> 525

<212> PRT

<213> Theobroma cacao

<400> 7

Met	Val	Ile	Ser	Lys	Ser	Pro	Phe	Ile	Val	Leu	Ile	Phe	Ser	Leu	Leu
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Leu	Ser	Phe	Ala	Leu	Leu	Cys	Ser	Gly	Val	Ser	Ala	Tyr	Gly	Arg	Lys
			20					25					30		
Gln	Tyr	Glu	Arg	Asp	Pro	Arg	Gln	Gln	Tyr	Glu	Gln	Cys	Gln	Arg	Arg
		35					40					45			
Cys	Glu	Ser	Glu	Ala	Thr	Glu	Glu	Arg	Glu	Gln	Glu	Gln	Cys	Glu	Gln
	50					55					60				
Arg	Cys	Glu	Arg	Glu	Tyr	Lys	Glu	Gln	Gln	Arg	Gln	Gln	Glu	Glu	Glu
65					70					75					80
Leu	Gln	Arg	Gln	Tyr	Gln	Gln	Cys	Gln	Gly	Arg	Cys	Gln	Glu	Gln	Gln
			85						90					95	
Gln	Gly	Gln	Arg	Glu	Gln	Gln	Gln	Cys	Gln	Arg	Lys	Cys	Trp	Glu	Gln
			100					105					110		
Tyr	Lys	Glu	Gln	Glu	Arg	Gly	Glu	His	Glu	Asn	Tyr	His	Asn	His	Lys
		115					120					125			
Lys	Asn	Arg	Ser	Glu	Glu	Glu	Glu	Gly	Gln	Gln	Arg	Asn	Asn	Pro	Tyr
	130					135					140				
Tyr	Phe	Pro	Lys	Arg	Arg	Ser	Phe	Gln	Thr	Arg	Phe	Arg	Asp	Glu	Glu
145					150					155					160
Gly	Asn	Phe	Lys	Ile	Leu	Gln	Arg	Phe	Ala	Glu	Asn	Ser	Pro	Pro	Leu
			165						170					175	
Lys	Gly	Ile	Asn	Asp	Tyr	Arg	Leu	Ala	Met	Phe	Glu	Ala	Asn	Pro	Asn
			180					185					190		
Thr	Phe	Ile	Leu	Pro	His	His	Cys	Asp	Ala	Glu	Ala	Ile	Tyr	Phe	Val
	195						200					205			
Thr	Asn	Gly	Lys	Gly	Thr	Ile	Thr	Phe	Val	Thr	His	Glu	Asn	Lys	Glu
	210					215					220				
Ser	Tyr	Asn	Val	Gln	Arg	Gly	Thr	Val	Val	Ser	Val	Pro	Ala	Gly	Ser
225					230					235					240
Thr	Val	Tyr	Val	Val	Ser	Gln	Asp	Asn	Gln	Glu	Lys	Leu	Thr	Ile	Ala
			245						250					255	
Val	Leu	Ala	Leu	Pro	Val	Asn	Ser	Pro	Gly	Lys	Tyr	Glu	Leu	Phe	Phe
		260						265					270		
Pro	Ala	Gly	Asn	Asn	Lys	Pro	Glu	Ser	Tyr	Tyr	Gly	Ala	Phe	Ser	Tyr
	275					280						285			
Glu	Val	Leu	Glu	Thr	Val	Phe	Asn	Thr	Gln	Arg	Glu	Lys	Leu	Glu	Glu
	290					295					300				
Ile	Leu	Glu	Glu	Gln	Arg	Gly	Gln	Lys	Arg	Gln	Gln	Gly	Gln	Gln	Gly
305					310					315					320
Met	Phe	Arg	Lys	Ala	Lys	Pro	Glu	Gln	Ile	Arg	Ala	Ile	Ser	Gln	Gln
			325						330					335	
Ala	Thr	Ser	Pro	Arg	His	Arg	Gly	Gly	Glu	Arg	Leu	Ala	Ile	Asn	Leu
			340					345					350		
Leu	Ser	Gln	Ser	Pro	Val	Tyr	Ser	Asn	Gln	Asn	Gly	Arg	Phe	Phe	Glu
		355					360					365			
Ala	Cys	Pro	Glu	Asp	Phe	Ser	Gln	Phe	Gln	Asn	Met	Asp	Val	Ala	Val
	370					375					380				
Ser	Ala	Phe	Lys	Leu	Asn	Gln	Gly	Ala	Ile	Phe	Val	Pro	His	Tyr	Asn
385					390					395					400
Ser	Lys	Ala	Thr	Phe	Val	Val	Phe	Val	Thr	Asp	Gly	Tyr	Gly	Tyr	Ala
			405						410					415	
Gln	Met	Ala	Cys	Pro	His	Leu	Ser	Arg	Gln	Ser	Gln	Gly	Ser	Gln	Ser

290		295		300
Phe Glu Glu Phe Phe Pro Ala Gly Ser Gln Arg Pro Gln Ser Tyr Leu				
305		310		320
Arg Ala Phe Ser Arg Glu Ile Leu Glu Pro Ala Phe Asn Thr Arg Ser				
	325		330	335
Glu Gln Leu Asp Glu Leu Phe Gly Gly Arg Gln Ser Arg Arg Arg Gln				
	340		345	350
Gln Gly Gln Gly Met Phe Arg Lys Ala Ser Gln Glu Gln Ile Arg Ala				
	355		360	365
Leu Ser Gln Glu Ala Thr Ser Pro Arg Glu Lys Ser Gly Glu Arg Phe				
	370		375	380
Ala Phe Asn Leu Leu Ser Gln Thr Pro Arg Tyr Ser Asn Gln Asn Gly				
385		390		400
Arg Phe Phe Glu Ala Cys Pro Pro Glu Phe Arg Gln Leu Arg Asp Ile				
	405		410	415
Asn Val Thr Val Ser Ala Leu Gln Leu Asn Gln Gly Ser Ile Phe Val				
	420		425	430
Pro His Tyr Asn Ser Lys Ala Thr Phe Val Ile Leu Val Thr Glu Gly				
	435		440	445
Asn Gly Tyr Ala Glu Met Val Ser Pro His Leu Pro Arg Gln Ser Ser				
	450		455	460
Tyr Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Gln Glu Gln Glu				
465		470		480
Glu Glu Arg Arg Ser Gly Gln Tyr Arg Lys Ile Arg Ser Arg Leu Ser				
	485		490	495
Arg Gly Asp Ile Phe Val Val Pro Ala Asn Phe Pro Val Thr Phe Val				
	500		505	510
Ala Ser Gln Asn Gln Asn Leu Arg Met Thr Gly Phe Gly Leu Tyr Asn				
	515		520	525
Gln Asn Ile Asn Pro Asp His Asn Gln Arg Ile Phe Val Ala Gly Lys				
	530		535	540
Ile Asn His Val Arg Gln Trp Asp Ser Gln Ala Lys Glu Leu Ala Phe				
545		550		560
Gly Val Ser Ser Arg Leu Val Asp Glu Ile Phe Asn Ser Asn Pro Gln				
	565		570	575
Glu Ser Tyr Phe Val Ser Arg Gln Arg Gln Arg Ala Ser Glu				
	580		585	590

<210> 9
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide 1 from *M. integrifolia* MiAMP2c in which
 Cys is replaced with Ala and Tyr is replaced with
 Ala, MiAMP2cpep1.

<400> 9
Arg Gln Arg Asp Pro Gln Gln Gln Ala Glu Gln Ala Gln Lys Arg Ala
1 5 10 15
Gln Arg Arg Glu Thr Glu
20

<210> 10
 <211> 25
 <212> PRT

<213> Artificial Sequence

<220>

<223> Peptide 2 from *M. integrifolia* MiAMP2c,
MiAMPcpep2.

<400> 10
Pro Arg His Met Gln Ile Ala Gln Gln Arg Ala Glu Arg Arg Ala Glu
1 5 10 15
Lys Glu Lys Arg Lys Gln Gln Lys Arg
20 25

<210> 11
<211> 36
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic DNA sequence coding for a leader
peptide.

<400> 11
Ser Glu Gln Ile Asp Asn Met Ala Trp Phe His Val Ser Val Cys Asn
1 5 10 15
Ala Val Phe Val Val Ile Ile Ile Ile Met Leu Leu Met Phe Val Pro
20 25 30
Val Val Arg Gly
35

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer JPM17 which binds to *M. integrifolia*
MiAMP2c.

<400> 12
cagcagcagt atgagcagtg 20

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer JMP20, a degenerate primer that binds to
MiAMP2-like sequences.

<400> 13
tttttcgtak ckkckttcgc a 21

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
 <223> Primer JPM31 corresponding to the 5' coding region
 of MiAMP2c and containing NdeI and BamHI sites.

<400> 14
 acaccatatg cgacaacgtg atcc 24

<210> 15
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer JPM32 corresponding to the 3' coding region
 of MiAMP2c and containing NdeI and BamHI sites.

<400> 15
 cgttgttttc tctattccta gggttg 26

<210> 16
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide containing His tag and Factor Xa cleavage
 site of PET16b vector.

<400> 16
 Met Gly His His His His His His His His His Ser Ser Gly His
 1 5 10 15
 Ile Glu Gly Arg His Met
 20

<210> 17
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TcAMP1 forward oligonucleotide.

<400> 17
 gggaattcca tatgtatgag cgtgatcctc gacagcaata cgagcaatgc cagaggcgat 60
 gcgagtcgga agcgactgaa gaaagggagc 90

<210> 18
 <211> 91
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TcAMP1 reverse oligonucleotide.

<400> 18
 gaagcgactg aagaaagggg gcaagagcag tgtgaacaac gctgtgaaag ggagtacaag 60

gagcagcaga gacagcaata gggatccaca c

91

<210> 19

<211> 101

<212> DNA

<213> Artificial Sequence

<220>

<223> TcAMP2 forward oligonucleotide.

<400> 19

gggaattcca tatgcttcaa aggcaatacc agcaatgtca agggcggttgt caagagcaac
aacaggggca gagagagcag cagcagtgcc agagaaaatg c

60

101

<210> 20

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> TcAMP2 reverse oligonucleotide.

<400> 20

gtgtggatcc ctagctccta ttttttttgt gattatggta attctcgtgc tcgcctctct
cttggttcctt atattgctcc cagcattttc tctggcactg ct

60

102

<210> 21

<211> 614

<212> PRT

<213> Peanut

<400> 21

Met	Arg	Gly	Arg	Val	Ser	Pro	Leu	Met	Leu	Leu	Leu	Gly	Ile	Leu	Val
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Leu	Ala	Ser	Val	Ser	Ala	Thr	Gln	Ala	Lys	Ser	Pro	Tyr	Arg	Lys	Thr
			20					25					30		
Glu	Asn	Pro	Cys	Ala	Gln	Arg	Cys	Leu	Gln	Ser	Cys	Gln	Gln	Glu	Pro
		35					40					45			
Asp	Asp	Leu	Lys	Gln	Lys	Ala	Cys	Glu	Ser	Arg	Cys	Thr	Lys	Leu	Glu
	50				55						60				
Tyr	Asp	Pro	Arg	Cys	Val	Tyr	Asp	Thr	Gly	Ala	Thr	Asn	Gln	Arg	His
65					70					75				80	
Pro	Pro	Gly	Glu	Arg	Thr	Arg	Gly	Arg	Gln	Pro	Gly	Asp	Tyr	Asp	Asp
				85					90					95	
Asp	Arg	Arg	Gln	Pro	Arg	Arg	Glu	Glu	Gly	Gly	Arg	Trp	Gly	Pro	Ala
			100					105					110		
Glu	Pro	Arg	Glu	Arg	Glu	Arg	Glu	Glu	Asp	Trp	Arg	Gln	Pro	Arg	Glu
		115					120					125			
Asp	Trp	Arg	Arg	Pro	Ser	His	Gln	Gln	Pro	Arg	Lys	Ile	Arg	Pro	Glu
	130					135					140				
Gly	Arg	Glu	Gly	Glu	Gln	Glu	Trp	Gly	Thr	Pro	Gly	Ser	Glu	Val	Arg
145					150					155				160	
Glu	Glu	Thr	Ser	Arg	Asn	Asn	Pro	Phe	Tyr	Phe	Pro	Ser	Arg	Arg	Phe
			165						170					175	
Ser	Thr	Arg	Tyr	Gly	Asn	Gln	Asn	Gly	Arg	Ile	Arg	Val	Leu	Gln	Arg
			180					185					190		
Phe	Asp	Gln	Arg	Ser	Lys	Gln	Phe	Gln	Asn	Leu	Gln	Asn	His	Arg	Ile

Met 1	Val	Ser	Ala	Arg 5	Ile	Val	Val	Leu	Leu 10	Ala	Thr	Leu	Leu	Cys 15	Ala
Ala	Ala	Ala	Val	Ala	Ser	Ser	Trp	Glu	Asp	Asp	Asn	His	His	His	His
			20					25				30			
Gly	Gly	His	Lys	Ser	Gly	Gln	Cys	Val	Arg	Arg	Cys	Glu	Asp	Arg	Pro
		35				40					45				
Trp	His	Gln	Arg	Pro	Arg	Cys	Leu	Glu	Gln	Cys	Arg	Glu	Glu	Glu	Arg
	50				55					60					
Glu	Lys	Arg	Gln	Glu	Arg	Ser	Arg	His	Glu	Ala	Asp	Asp	Arg	Ser	Gly
65				70				75						80	
Glu	Gly	Ser	Ser	Glu	Asp	Glu	Arg	Glu	Gln	Glu	Lys	Glu	Lys	Gln	Lys
			85					90					95		
Asp	Arg	Arg	Pro	Tyr	Val	Phe	Asp	Arg	Arg	Ser	Phe	Arg	Arg	Val	Val
			100				105					110			
Arg	Ser	Glu	Gln	Gly	Ser	Leu	Arg	Val	Leu	Arg	Pro	Phe	Asp	Glu	Val
		115				120					125				
Ser	Arg	Leu	Leu	Arg	Gly	Ile	Arg	Asp	Tyr	Arg	Val	Ala	Val	Leu	Glu
	130				135			140							
Ala	Asn	Pro	Arg	Ser	Phe	Val	Val	Pro	Ser	His	Thr	Asp	Ala	His	Cys
145				150				155						160	
Ile	Cys	Tyr	Val	Ala	Glu	Gly	Glu	Gly	Val	Val	Thr	Thr	Ile	Glu	Asn
			165				170						175		
Gly	Glu	Arg	Arg	Ser	Tyr	Thr	Ile	Lys	Gln	Gly	His	Val	Phe	Val	Ala
		180				185						190			
Pro	Ala	Gly	Ala	Val	Thr	Tyr	Leu	Ala	Asn	Thr	Asp	Gly	Arg	Lys	Lys
		195				200					205				
Leu	Val	Ile	Thr	Lys	Ile	Leu	His	Thr	Ile	Ser	Val	Pro	Gly	Glu	Phe
	210			215						220					
Gln	Phe	Phe	Phe	Gly	Pro	Gly	Gly	Arg	Asn	Pro	Glu	Ser	Phe	Leu	Ser
225				230					235					240	
Ser	Phe	Ser	Lys	Ser	Ile	Gln	Arg	Ala	Ala	Tyr	Lys	Thr	Ser	Ser	Asp
			245					250					255		
Arg	Leu	Glu	Arg	Leu	Phe	Gly	Arg	His	Gly	Gln	Asp	Lys	Gly	Ile	Ile
			260				265					270			
Val	Arg	Ala	Thr	Glu	Glu	Gln	Thr	Arg	Glu	Leu	Arg	Arg	His	Ala	Ser
		275				280					285				
Glu	Gly	Gly	His	Gly	Pro	His	Trp	Pro	Leu	Pro	Pro	Phe	Gly	Glu	Ser
	290				295					300					
Arg	Gly	Pro	Tyr	Ser	Leu	Leu	Asp	Gln	Arg	Pro	Ser	Ile	Ala	Asn	Gln
305				310				315						320	
His	Gly	Gln	Leu	Tyr	Glu	Ala	Asp	Ala	Arg	Ser	Phe	His	Asp	Leu	Ala
			325					330					335		
Glu	His	Asp	Val	Ser	Val	Ser	Phe	Ala	Asn	Ile	Thr	Ala	Gly	Ser	Met
			340				345					350			
Ser	Ala	Pro	Leu	Phe	Asn	Thr	Arg	Ser	Phe	Lys	Ile	Ala	Tyr	Val	Pro
		355	</												

Ala	Gly	His	Pro	Phe	Val	Ala	Val	Ala	Ser	Arg	Asp	Ser	Asn	Leu	Gln
		435						440				445			
Ile	Val	Cys	Phe	Glu	Val	His	Ala	Asp	Arg	Asn	Glu	Lys	Val	Phe	Leu
	450					455					460				
Ala	Gly	Ala	Asp	Asn	Val	Leu	Gln	Lys	Leu	Asp	Arg	Val	Ala	Lys	Ala
465					470					475					480
Leu	Ser	Phe	Ala	Ser	Lys	Ala	Glu	Glu	Val	Asp	Glu	Val	Leu	Gly	Ser
				485						490				495	
Arg	Arg	Glu	Lys	Gly	Phe	Leu	Pro	Gly	Pro	Glu	Glu	Ser	Gly	Gly	His
			500					505					510		
Glu	Glu	Arg	Glu	Gln	Glu	Glu	Glu	Arg	Glu	Glu	Arg	His	Gly	Gly	
		515					520					525			
Arg	Gly	Glu	Arg	Glu	Arg	His	Gly	Arg	Glu	Glu	Arg	Glu	Lys	Glu	Glu
	530					535					540				
Glu	Arg	Glu	Gly	Arg	His	Gly	Gly	Arg	Glu	Glu	Arg	Glu	Glu	Glu	Glu
545					550					555					560
Arg	His	Gly	Arg	Gly	Arg	Arg	Glu	Glu	Val	Ala	Glu	Thr	Leu	Met	Arg
				565					570					575	
Met	Val	Thr	Ala	Arg	Met										
				580											

<210> 23
 <211> 33
 <212> PRT
 <213> Maize

<400> 23

Arg	Ser	Gly	Arg	Gly	Glu	Cys	Arg	Arg	Gln	Cys	Leu	Arg	Arg	His	Glu
1				5					10					15	
Gly	Gln	Pro	Trp	Glu	Thr	Gln	Glu	Cys	Met	Arg	Arg	Cys	Arg	Arg	Arg
			20					25					30		

Gly

<210> 24
 <211> 637
 <212> PRT
 <213> Barley

<400> 24

Met	Ala	Thr	Arg	Ala	Lys	Ala	Thr	Ile	Pro	Leu	Leu	Phe	Leu	Leu	Gly
1				5					10					15	
Thr	Ser	Leu	Leu	Phe	Ala	Ala	Ala	Val	Ser	Ala	Ser	His	Asp	Asp	Glu
			20					25					30		
Asp	Asp	Arg	Arg	Gly	Gly	His	Ser	Leu	Gln	Gln	Cys	Val	Gln	Arg	Cys
	35					40						45			
Arg	Gln	Glu	Arg	Pro	Arg	Tyr	Ser	His	Ala	Arg	Cys	Val	Gln	Glu	Cys
	50					55				60					
Arg	Asp	Asp	Gln	Gln	Gln	His	Gly	Arg	His	Glu	Gln	Glu	Glu	Glu	Gln
65					70					75					80
Gly	Arg	Gly	Arg	Gly	Trp	His	Gly	Glu	Gly	Glu	Arg	Glu	Glu	Glu	His
				85				90					95		
Gly	Arg	Gly	Arg	Gly	Arg	His	Gly	Glu	Gly	Glu	Arg	Glu	Glu	Glu	His
			100				105					110			
Gly	Arg	Gly	Arg	Gly	Arg	His	Gly	Glu	Gly	Glu	Arg	Glu	Glu	Glu	Arg
	115						120					125			
Gly	Arg	Gly	His	Gly	Arg	His	Gly	Glu	Gly	Glu	Arg	Glu	Glu	Glu	Arg

130		135		140
Gly Arg Gly Arg Gly Arg	His Gly Glu Gly Glu Arg	Glu Arg Glu Glu Glu Glu		
145	150	155	160	
Gly Arg Gly Arg Gly Arg	Arg Gly Glu Gly Glu Arg	Asp Glu Glu Gln		
165	170	175		
Gly Asp Ser Arg Arg Pro	Tyr Val Phe Gly Pro Arg	Ser Phe Arg Arg		
180	185	190		
Ile Ile Gln Ser Asp His	Gly Phe Val Arg Ala Leu	Arg Pro Phe Asp		
195	200	205		
Gln Val Ser Arg Leu Leu	Arg Gly Ile Arg Asp Tyr	Arg Val Ala Ile		
210	215	220		
Met Glu Val Asn Pro Arg	Ala Phe Val Val Pro Gly	Phe Thr Asp Ala		
225	230	235	240	
Asp Gly Val Gly Tyr Val	Ala Gln Gly Glu Gly Val	Leu Thr Val Ile		
245	250	255		
Glu Asn Gly Glu Lys Arg	Ser Tyr Thr Val Lys Glu	Gly Asp Val Ile		
260	265	270		
Val Ala Pro Ala Gly Ser	Ile Met His Leu Ala Asn	Thr Asp Gly Arg		
275	280	285		
Arg Lys Leu Val Ile Ala	Lys Ile Leu His Thr Ile	Ser Val Pro Gly		
290	295	300		
Lys Phe Gln Phe Leu Ser	Val Lys Pro Leu Leu Ala	Ser Leu Ser Lys		
305	310	315	320	
Arg Val Leu Arg Ala Ala	Phe Lys Thr Ser Asp Glu	Arg Leu Glu Arg		
325	330	335		
Leu Phe Asn Gln Arg Gln	Gly Gln Glu Lys Thr Arg	Ser Val Ser Ile		
340	345	350		
Val Arg Ala Ser Glu Glu	Gln Leu Arg Glu Leu Arg	Arg Glu Ala Ala		
355	360	365		
Glu Gly Gly Gln Gly His	Arg Trp Pro Leu Pro Pro	Phe Arg Gly Asp		
370	375	380		
Ser Arg Asp Thr Phe Asn	Leu Leu Glu Gln Arg Pro	Lys Ile Ala Asn		
385	390	395	400	
Arg His Gly Arg Leu Tyr	Glu Ala Asp Ala Arg Ser	Phe His Ala Leu		
405	410	415		
Ala Asn Gln Asp Val Arg	Val Ala Asn Ile Thr Pro	Gly Ser		
420	425	430		
Met Thr Ala Pro Tyr Leu	Asn Thr Gln Ser Phe Lys	Leu Ala Val Val		
435	440	445		
Leu Glu Gly Glu Gly Glu	Val Gln Ile Val Cys Pro	His Leu Gly Arg		
450	455	460		
Glu Ser Glu Ser Glu Arg	Glu His Gly Lys Gly Arg	Arg Arg Glu Glu		
465	470	475	480	
Glu Glu Asp Asp Gln Arg	Gln Gln Arg Arg Gly Ser	Glu Ser Glu		
485	490	495		
Ser Glu Glu Glu Glu Glu	Gln Gln Arg Tyr Glu Thr	Val Arg Ala Arg		
500	505	510		
Val Ser Arg Gly Ser Ala	Phe Val Val Pro Pro Gly	His Pro Val Val		
515	520	525		
Glu Ile Ser Ser Ser Gln	Gly Ser Ser Asn Leu Gln	Val Val Cys Phe		
530	535	540		
Glu Ile Asn Ala Glu Arg	Asn Glu Arg Val Trp Leu	Ala Gly Arg Asn		
545	550	555	560	
Asn Val Ile Gly Lys Leu	Gly Ser Pro Ala Gln Glu	Leu Thr Phe Gly		
565	570	575		
Arg Pro Ala Arg Glu Val	Gln Glu Val Phe Arg Ala	Gln Asp Gln Asp		
580	585	590		

Glu	Gly	Phe	Val	Ala	Gly	Pro	Glu	Gln	Gln	Ser	Arg	Glu	Gln	Glu	Gln
		595					600					605			
Glu	Gln	Glu	Arg	His	Arg	Arg	Arg	Gly	Asp	Arg	Gly	Arg	Gly	Asp	Glu
	610						615				620				
Ala	Val	Glu	Thr	Phe	Leu	Arg	Met	Ala	Thr	Gly	Ala	Ile			
625					630					635					

<210> 25
 <211> 605
 <212> PRT
 <213> Soybean (Glycine max)

<400> 25

Met	Met	Arg	Ala	Arg	Phe	Pro	Leu	Leu	Leu	Leu	Gly	Leu	Val	Phe	Leu
1				5					10					15	
Ala	Ser	Val	Ser	Val	Ser	Phe	Gly	Ile	Ala	Tyr	Trp	Glu	Lys	Glu	Asn
		20						25					30		
Pro	Lys	His	Asn	Lys	Cys	Leu	Gln	Ser	Cys	Asn	Ser	Glu	Arg	Asp	Ser
		35					40					45			
Tyr	Arg	Asn	Gln	Ala	Cys	His	Ala	Arg	Cys	Asn	Leu	Leu	Lys	Val	Glu
	50					55					60				
Lys	Glu	Glu	Cys	Glu	Glu	Gly	Glu	Ile	Pro	Arg	Pro	Arg	Pro	Arg	Pro
65					70					75					80
Gln	His	Pro	Glu	Arg	Glu	Pro	Gln	Gln	Pro	Gly	Glu	Lys	Glu	Glu	Asp
				85					90					95	
Glu	Asp	Glu	Gln	Pro	Arg	Pro	Ile	Pro	Phe	Pro	Arg	Pro	Gln	Pro	Arg
		100						105					110		
Gln	Glu	Glu	Glu	His	Glu	Gln	Arg	Glu	Glu	Gln	Glu	Trp	Pro	Arg	Lys
		115				120						125			
Glu	Glu	Lys	Arg	Gly	Glu	Lys	Gly	Ser	Glu	Glu	Glu	Asp	Glu	Asp	Glu
	130					135					140				
Asp	Glu	Glu	Gln	Asp	Glu	Arg	Gln	Phe	Pro	Phe	Pro	Arg	Pro	Pro	His
145					150					155					160
Gln	Lys	Glu	Glu	Arg	Asn	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Gln	Gln
				165					170					175	
Arg	Glu	Ser	Glu	Glu	Ser	Glu	Asp	Ser	Glu	Leu	Arg	Arg	His	Lys	Asn
		180					185						190		
Lys	Asn	Pro	Phe	Leu	Phe	Gly	Ser	Asn	Arg	Phe	Glu	Thr	Leu	Phe	Lys
	195					200						205			
Asn	Gln	Tyr	Gly	Arg	Ile	Arg	Val	Leu	Gln	Arg	Phe	Asn	Gln	Arg	Ser
	210				215						220				
Pro	Gln	Leu	Gln	Asn	Leu	Arg	Asp	Tyr	Arg	Ile	Leu	Glu	Phe	Asn	Ser
225					230					235					240
Lys	Pro	Asn	Thr	Leu	Leu	Pro	Asn	His	Ala	Asp	Ala	Asp	Tyr	Leu	
			245					250					255		
Ile	Val	Ile	Leu	Asn	Gly	Thr	Ala	Ile	Leu	Ser	Leu	Val	Asn	Asn	Asp
		260						265					270		
Asp	Arg	Asp	Ser	Tyr	Arg	Leu	Gln	Ser	Gly	Asp	Ala	Leu	Arg	Val	Pro
		275					280					285			
Ser	Gly	Thr	Thr	Tyr	Tyr	Val	Val	Asn	Pro	Asp	Asn	Asn	Glu	Asn	Leu
	290					295					300				
Arg	Leu	Ile	Thr	Leu	Ala	Ile	Pro	Val	Asn	Lys	Pro	Gly	Arg	Phe	Glu
305					310					315					320
Ser	Phe	Phe	Leu	Ser	Ser	Thr	Glu	Ala	Gln	Gln	Ser	Tyr	Leu	Gln	Gly
				325					330					335	
Phe	Ser	Arg	Asn	Ile	Leu	Glu	Ala	Ser	Tyr	Asp	Thr	Lys	Phe	Glu	Glu
			340					345					350		

Ile Asn Lys Val Leu Phe Ser Arg Glu Glu Gly Gln Gln Gln Gly Glu
 355 360 365
 Gln Arg Leu Gln Glu Ser Val Ile Val Glu Ile Ser Lys Glu Gln Ile
 370 375 380
 Arg Ala Leu Ser Lys Arg Ala Lys Ser Ser Ser Arg Lys Thr Ile Ser
 385 390 395 400
 Ser Glu Asp Lys Pro Phe Asn Leu Arg Ser Arg Asp Pro Ile Tyr Ser
 405 410 415
 Asn Lys Leu Gly Lys Phe Phe Glu Ile Thr Pro Glu Lys Asn Pro Gln
 420 425 430
 Leu Arg Asp Leu Asp Ile Phe Leu Ser Ile Val Asp Met Asn Glu Gly
 435 440 445
 Ala Leu Leu Leu Pro His Phe Asn Ser Lys Ala Ile Val Ile Leu Val
 450 455 460
 Ile Asn Glu Gly Asp Ala Asn Ile Glu Leu Val Gly Leu Lys Glu Gln
 465 470 475 480
 Gln Gln Glu Gln Gln Gln Glu Glu Gln Pro Leu Glu Val Arg Lys Tyr
 485 490 495
 Arg Ala Glu Leu Ser Glu Gln Asp Ile Phe Val Ile Pro Ala Gly Tyr
 500 505 510
 Pro Val Val Val Asn Ala Thr Ser Asn Leu Asn Phe Phe Ala Ile Gly
 515 520 525
 Ile Asn Ala Glu Asn Asn Gln Arg Asn Phe Leu Ala Gly Ser Gln Asp
 530 535 540
 Asn Val Ile Ser Gln Ile Pro Ser Gln Val Gln Glu Leu Ala Phe Pro
 545 550 555 560
 Gly Ser Ala Gln Ala Val Glu Lys Leu Leu Lys Asn Gln Arg Glu Ser
 565 570 575
 Tyr Phe Val Asp Ala Gln Pro Lys Lys Glu Glu Gly Asn Lys Gly
 580 585 590
 Arg Lys Gly Pro Leu Ser Ser Ile Leu Arg Ala Phe Tyr
 595 600 605

<210> 26
 <211> 23
 <212> PRT
 <213> Stenocarpus sinuatus

<220>
 <221> PEPTIDE
 <222> (1)...(23)
 <223> Partial MiAMP2c homologous peptide.

<400> 26
 Val Lys Glu Asp His Gln Phe Glu Thr Arg Gly Glu Ile Leu Glu Cys
 1 5 10 15
 Tyr Arg Leu Cys Gln Gln Gln
 20

<210> 27
 <211> 17
 <212> PRT
 <213> Stenocarpus sinuatus

<220>
 <221> PEPTIDE
 <222> (1)...(27)

<223> Partial MiAMP2c homologous peptide.

<400> 27
Gln Lys His Arg Ser Gln Ile Leu Gly Cys Tyr Leu Xaa Cys Gln Gln Leu
1 5 10 15

<210> 28
<211> 28
<212> PRT
<213> Stenocarpus sinuatus

<220>
<221> PEPTIDE
<222> (1)...(28)
<223> Partial MiAMP2c homologous peptide.

<400> 28
Leu Asp Pro Ile Arg Gln Gln Gln Leu Cys Gln Met Arg Cys Gln Gln
1 5 10 15
Gln Glu Lys Asp Pro Arg Gln Gln Gln Gln Cys Lys
20 25

<210> 29
<211> 368
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic nucleotide sequence which can be used
for the expression and secretion of MiAMP2c,
containing the leader sequence from SEQ ID NO:11
and SEQ ID NO:5.

<221> CDS
<222> (103)...(333)

<400> 29
aactctagag cggcgcgctc gactatTTTTT acaacaatta ccaacaacaa caaacaacaa 60
acaacattac aattactatt tacaattaca ggatccacaa ca atg gct tgg ttc 114
Met Ala Trp Phe
1

cac gtt tct gtt tgt aac gct gtt ttc gtt gtt att att att att atg 162
His Val Ser Val Cys Asn Ala Val Phe Val Val Ile Ile Ile Ile Met
5 10 15 20

ctt ctt atg ttc gtt cct gtt gtt aga ggt aga caa aga gat cct caa 210
Leu Leu Met Phe Val Pro Val Val Arg Gly Arg Gln Arg Asp Pro Gln
25 30 35

caa caa tac gag caa tgt caa aag agg tgt caa agg aga gag act gag 258
Gln Gln Tyr Glu Gln Cys Gln Lys Arg Cys Gln Arg Arg Glu Thr Glu
40 45 50

cct aga cac atg caa att tgt cag caa agg tgt gaa agg agg tac gag 306
Pro Arg His Met Gln Ile Cys Gln Gln Arg Cys Glu Arg Arg Tyr Glu
55 60 65

aag gag aag agg aag caa caa aag agg tgaggatccg tcgacgcggc 353
 Lys Glu Lys Arg Lys Gln Gln Lys Arg
 70 75

cgcagatcta gacaa 368

<210> 30
 <211> 77
 <212> PRT
 <213> Artificial Sequence

<220>

<223> A synthetic peptide sequence which can be used for the expression and secretion of MiAMP2c containing the leader sequence from SEQ ID NO:11 and peptide sequence from SEQ ID NO:5.

<400> 30
 Met Ala Trp Phe His Val Ser Val Cys Asn Ala Val Phe Val Val Ile
 1 5 10 15
 Ile Ile Ile Met Leu Leu Met Phe Val Pro Val Val Arg Gly Arg Gln
 20 25 30
 Arg Asp Pro Gln Gln Gln Tyr Glu Gln Cys Gln Lys Arg Cys Gln Arg
 35 40 45
 Arg Glu Thr Glu Pro Arg His Met Gln Ile Cys Gln Gln Arg Cys Glu
 50 55 60
 Arg Arg Tyr Glu Lys Glu Lys Arg Lys Gln Gln Lys Arg
 65 70 75

<210> 31
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Consensus sequence for antimicrobial peptides wherein X is any amino acid.

<400> 31
 Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys
 20 25

<210> 32
 <211> 28
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Consensus sequence for antimicrobial peptides wherein X is any amino acid.

<400> 32
 Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys
 20 25

<210> 33
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence for antimicrobial peptides
 wherein X is any amino acid.

<400> 33
 Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys
 20 25

<210> 34
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence for antimicrobial peptides,
 wherein X is any amino acid and the first and
 last X are Phenylalanine or Tyrosine.

<400> 34
 Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
 20 25

<210> 35
 <211> 28
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence for antimicrobial peptides
 wherein X is any amino acid and the first and last
 X are phenylalanine or Tyrosine.

<400> 35
 Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
 20 25

<210> 36
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence for antimicrobial peptides

wherein X is any amino acid and the first and last X are phenylalanine or Tyrosine.

<400> 36
Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
20 25

<210> 37
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for antimicrobial peptides
wherein X is any amino acid.

<400> 37
Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1 5 10 15
Xaa Xaa Xaa Cys
20

<210> 38
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for antimicrobial peptides
wherein X is any amino acid.

<400> 38
Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Cys Xaa Xaa Xaa Cys
20

<210> 39
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for antimicrobial peptides
wherein X is any amino acid.

<400> 39
Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Cys Xaa Xaa Xaa Cys
20

<210> 40
<211> 5
<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence for antimicrobial peptides
wherein X is any amino acid.

<400> 40

Cys	Xaa	Xaa	Xaa	Cys
1				5